

04/25

#2



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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/074,596

DATE: 03/01/2002
TIME: 10:54:34

Input Set : A:\Clfr007.app
Output Set: N:\CRF3\03012002\J074596.raw

3 <110> APPLICANT: ROSENBLUM, MICHAEL G.
4 CHEUNG, LAWRENCE
6 <120> TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
7 MAKING THEEOF
9 <130> FILE REFERENCE: CLFR:007US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/074,596
12 <141> CURRENT FILING DATE: 2002-02-12
14 <150> PRIOR APPLICATION NUMBER: 60/268,402
15 <151> PRIOR FILING DATE: 2001-02-12
17 <160> NUMBER OF SEQ ID NOS: 11
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 316
23 <212> TYPE: PRT
24 <213> ORGANISM: Gelonium multiflorum
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29 Trp Phe Cys Cys Thr Thr Ile Val Leu Gly Ser Thr Ala Arg Ile Phe
30 20 25 30
31 Ser Leu Pro Thr Asn Asp Glu Glu Glu Thr Ser Lys Thr Leu Gly Leu
32 35 40 45
33 Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr Tyr Val
34 50 55 60
35 Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly Asn Ser
36 65 70 75 80
37 His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly Lys Cys
38 85 90 95
39 Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala Glu Ile
40 100 105 110
41 Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val Arg Asn
42 115 120 125
43 Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu Gly Leu
44 130 135 140
45 Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser Tyr Pro
46 145 150 155 160
47 Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu Gly Ile
48 165 170 175
49 Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala Ile Asp
50 180 185 190
51 Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val Ile Gln
52 195 200 205
53 Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln Ile Arg
54 210 215 220

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67 210 215 220
 69 Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile Ser Leu
 70 225 230 235 240
 72 Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser Gly Ala
 73 245 250 255
 75 Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn Gly Lys
 76 260 265 270
 78 Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile Ala Leu
 79 275 280 285
 81 Leu Lys Phe Val Asp Lys Asp Pro Lys Thr Ser Leu Ala Ala Glu Leu
 82 290 295 300
 84 Ile Ile Gln Asn Tyr Glu Ser Leu Val Gly Phe Asp
 85 305 310 315
 88 <210> SEQ ID NO: 2
 89 <211> LENGTH: 1176
 90 <212> TYPE: DNA
 91 <213> ORGANISM: *Gelonium multiflorum*
 93 <400> SEQUENCE: 2
 94 cagcttctca cttgtttggg ataatgaaag ggaacatgaa ggtgtactgg attaagattg 60
 95 ctgtggcgac atgggtttgc tgcactacta ttgtacttgg atcaacggcg aggattttct 120
 96 ctcttcccac aaatgatgaa gaagaaaacca gtaagacgct tggcctggac accgtgagct 180
 97 ttagcaacta aggtgccact tatattacct acgtgaattt cttgaatgag ctacgagttt 240
 98 aattgaaacc cgaaggtaac agccatggaa tcccattgct ggcaaaaaaaaa tgtgatgatc 300
 99 ctggaaagtg tttcggtttt gtagcgtttt caaatgacaa tggacagttt gcggaaatag 360
 100 ctatagatgt tacaagtgtt tatgtgggtt gctatcaagt aagaaacaga tcttacttct 420
 101 ttaaagatgc tccagatgtc gcttacgaaag gccttctcaa aaacacaatt aaaacaagac 480
 102 ttcattttgg cggcagctat ccctcgctgg aaggtgagaa ggcataataga gagacaacag 540
 103 acttgggcat tgaaccatta aggattggca tcaagaaaact ttagtggatgatc 600
 104 attataaacc aacggagata gctagttctc tattgggtt tattcaatgt gtgtctgaag 660
 105 cagctcgatt caccttattt gagaacccaa ttagaaataa ctttcaacag agaattcgcc 720
 106 cggcgaataaa tacaatcagc cttgagaata aatggggtaa actctcggtt cagatccgg 780
 107 catcagggtgc aaatggaatg ttttggggc cagttgaattt ggaacgtgca aatggcaaaa 840
 108 aatactatgt caccgcgtt gatcaagttt aacccaaaat agcactctt aagttcgatc 900
 109 ataaaagatcc taaaacgagc cttgctgtt aattgataat ccagaactat gagtcattag 960
 110 tgggctttga ttagtacaac ttattgtgtt ttttatataat tataatgtatg atgccggg 1020
 111 atgtattggc cttcgtagct taaaataaagg catgaatatt tagcctcggtt ggtgtatcta 1080
 112 tcatgtgtt ttgtaaaact gccaatgtt atgttatcaa acagaaattt gcatgaatgtt 1140
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 117 <211> LENGTH: 33
 118 <212> TYPE: DNA
 119 <213> ORGANISM: *Homo sapiens*
 121 <400> SEQUENCE: 3
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 126 <211> LENGTH: 50
 127 <212> TYPE: DNA
 128 <213> ORGANISM: *Homo sapiens*
 130 <400> SEQUENCE: 4

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131 gccggagcct ggcttgcacg ctgccgctgg tggagccttt gatcatccag      50
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137 <213> ORGANISM: Homo sapiens
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144 <211> LENGTH: 30
145 <212> TYPE: DNA
146 <213> ORGANISM: Homo sapiens
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153 <211> LENGTH: 51
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
159 Primer
161 <400> SEQUENCE: 7
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166 <211> LENGTH: 33
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168 <213> ORGANISM: Artificial Sequence
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181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
185 Primer
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193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
199 <220> FEATURE:
200 <221> NAME/KEY: CDS
201 <222> LOCATION: (1)..(1521)

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Input Set : A:\Clfr007.app
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203 <400> SEQUENCE: 10 48
204 atg acg gac att gtg atg acc cag tct caa aaa ttc atg tcc aca tca
205 Met Thr Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser
206 1 5 10 15
208 gta gga gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg gat 96
209 Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp
210 20 25 30
212 act aat gta gcc tgg tat caa caa aaa cca ggg caa tct cct gaa cca 144
213 Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Glu Pro
214 35 40 45
216 ctg ctt ttc tcg gca tcc tac cgt tac act gga gtc cct gat cgc ttc 192
217 Leu Leu Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe
218 50 55 60
220 aca ggc agt gga tct ggg aca gat ttc act ctc acc atc agc aat gtg 240
221 Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val
222 65 70 75 80
224 cag tct gaa gac ttg gca gag tat ttc tgt cag caa tat aac agc tat 288
225 Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr
226 85 90 95
228 cct ctg acg ttc ggt gga ggc acc aag ctg gag atc aaa ggc tcc acc 336
229 Pro Leu Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr
230 100 105 110
232 agc ggc agc ggt aag cca ggc tcc ggc gaa ggc agc acc aaa ggc gaa 384
233 Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu
234 115 120 125
236 gtg aag gtt gag gag tct gga gga ggc ttg gtg caa cct gga gga tcc 432
237 Val Lys Val Glu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser
238 130 135 140
240 atg aaa ctc tcc tgt gtc tct gga ttc act ttc ggt aat tac tgg 480
241 Met Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe Gly Asn Tyr Trp
242 145 150 155 160
244 atg aac tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg att gca 528
245 Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Ile Ala
246 165 170 175
248 gaa att aga ttg aaa tcc aat aat ttt gca aga tat tat gcg gag tct 576
249 Glu Ile Arg Leu Lys Ser Asn Asn Phe Ala Arg Tyr Tyr Ala Glu Ser
250 180 185 190
252 gtg aaa ggg agg ttc acc atc tca aga gat gat tcc aaa agt agt gtc 624
253 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val
254 195 200 205
256 tac ctg caa atg atc aac cta aga gct gaa gat act ggc att tat tac 672
257 Tyr Leu Gln Met Ile Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr Tyr
258 210 215 220
260 tgt acc agt tat ggt aac tac gtt ggg cac tat ttt gac cac tgg ggc 720
261 Cys Thr Ser Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp Gly
262 225 230 235 240
264 caa ggc acc act ctc acc gtc tcc tca gct agc ggt ggc ggt ggc tcc 768
265 Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Gly Gly Gly Ser
266 245 250 255
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268	ggt cta gac acc gtg agc ttt agc act aaa ggt gcc act tat att acc	816
269	Gly Leu Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr	
270	260 265 270	
272	tac gtg aat ttc ttg aat gag cta cga gtt aaa ttg aaa ccc gaa ggt	864
273	Tyr Val Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly	
274	275 280 285	
276	aac agc cat gga atc cca ttg ctg cgc aaa aaa tgt gat gat cct gga	912
277	Asn Ser His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly	
278	290 295 300	
280	aag tgt ttc gtt ttg gta gcg ctt tca aat gac aat gga cag ttg gcg	960
281	Lys Cys Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala	
282	305 310 315 320	
284	gaa ata gct ata gat gtt aca agt gtt tat gtg gtg ggc tat caa gta	1008
285	Glu Ile Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val	
286	325 330 335	
288	aga aac aga tct tac ttc ttt aaa gat gct cca gat gct gct tac gaa	1056
289	Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu	
290	340 345 350	
292	ggc ctc ttc aaa aac aca att aaa aca aga ctt cat ttt ggc ggc agc	1104
293	Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser	
294	355 360 365	
296	tat ccc tcg ctg gaa ggt gag aag gca tat aga gag aca aca gac ttg	1152
297	Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu	
298	370 375 380	
300	ggc att gaa cca tta agg att ggc atc aag aaa ctt gat gaa aat gcg	1200
301	Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala	
302	385 390 395 400	
304	ata gac aat tat aaa cca acg gag ata gct agt tct cta ttg gtt gtt	1248
305	Ile Asp Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val	
306	405 410 415	
308	att caa atg gtg tct gaa gca gct cga ttc acc ttt att gag aac caa	1296
309	Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln	
310	420 425 430	
312	att aga aat aac ttt caa cag aga att cgc ccg gcg aat aat aca atc	1344
313	Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile	
314	435 440 445	
316	agc ctt gag aat aaa tgg ggt aaa ctc tcg ttc cag atc ccg aca tca	1392
317	Ser Leu Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser	
318	450 455 460	
320	ggt gca aat gga atg ttt tcg gag gca gtt gaa ttg gaa cgt gca aat	1440
321	Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn	
322	465 470 475 480	
324	ggc aaa aaa tac tat gtc acc gca gtt gat caa gta aaa ccc aaa ata	1488
325	Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile	
326	485 490 495	
328	gca ctc ttg aag ttc gtc gat aaa gat cct aaa taatga	1527
329	Ala Leu Leu Lys Phe Val Asp Lys Asp Pro Lys	
330	500 505	
333	<210> SEQ ID NO: 11	

VERIFICATION SUMMARY
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L:337 M:258 W: Mandatory Feature missing, <220> FEATURE: